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OM protein - protein search, using sw model

Run on January 16, 2003, 16:39:12, Search time 20.4 seconds  
(without alignments)  
28.464 Million cell updates/sec

Title: US-09-856-070-17  
Perfect score: 69  
Sequence: 1 ERKEQMMREKEEL 14

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Swissprot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	580	EZRI_HOVIN	P31976 bos taurus
2	69	100.0	585	EZRI_HOVIN	P15411 homo sapien
3	66	95.7	585	EZRI_HOVIN	P26040 mus muscula
4	51	73.9	576	MOES_MOUSE	P26038 homo sapien
5	51	73.9	576	MOES_MOUSE	P26041 mus muscula
6	51	73.9	576	MOES_MOUSE	P26042 sus scrofa
7	51	73.9	583	RADI_HUMAN	P35241 homo sapien
8	51	73.9	583	RADI_HUMAN	P26043 mus muscula
9	51	73.9	583	RADI_HUMAN	P26044 sus scrofa
10	47	68.1	1549	TRHY_SHEEP	P22793 ovis aries
11	46	66.7	2564	SPCQ_HUMAN	Q9H254 homo sapien
12	43	62.3	121	ABRA_FLATF	P23746 plasmodium
13	43	62.3	743	ABRA_FLATF	P22620 plasmodium
14	43	62.3	1157	V182_HUMAN	Q14487 homo sapien
15	43	62.3	1344	IF3A_MOUSE	P23116 mus muscula
16	43	62.3	1382	IF3A_HUMAN	Q14752 homo sapien
17	43	62.3	1407	TRHY_PABIT	P27709 oryza sativa
18	43	62.3	1808	TRHY_HUMAN	Q07383 homo sapien
19	42	60.9	123	RIFA_NEIMA	Q9J1X7 neisseria m
20	42	60.9	123	RIFA_NEIMA	Q9J1X2 neisseria m
21	42	60.9	216	PRP6_YEAST	P53198 saccharomyc
22	42	60.9	471	VAL5_SCHUG	Q93428 schizosacch
23	42	60.9	514	ZEP1_MOUSE	P54103 mus muscula
24	42	60.9	4587	EELI_RAT	P30427 fatius norv
25	41	59.4	85	IATP_YEAST	P01097 saccharomyc
26	41	59.4	243	TRIC_XENIA	P59754 xenopus lae
27	41	59.4	386	NISSC_HUMAN	Q9H116 homo sapien
28	41	59.4	419	NEMO_HUMAN	Q9Y649 h nf-kappa
29	41	59.4	476	MPPB_NEUCR	P11913 neurospora
30	41	59.4	877	INPE_HICOF	P43452 gallus gall
31	41	59.4	2068	TZDI_HUMAN	P51123 drosophila
32	40	58.0	180	PTTG_HUMAN	P53801 homo sapien
33	40	58.0	249	PSEL_MOUSE	P97371 mus muscula

34	40	58.0	462	1	MPPB_YEAST
35	40	58.0	466	1	CYP8_CAMEL
36	40	58.0	503	1	CP39_RAT
37	40	58.0	503	1	CP30_MOUSE
38	40	58.0	592	1	GP1_HUMAN
39	40	58.0	1459	1	MYH9_CHICK
40	40	58.0	1460	1	MYH9_HUMAN
41	40	58.0	4473	1	PIEL_CRICR
42	39	56.5	148	1	SSRP_RALSO
43	39	56.5	309	1	MATL_XENLA
44	39	56.5	330	1	RLX3_STRAU
45	39	56.5	341	1	12D6_MOUSE

## ALIGNMENTS

RESULT 1	EZRI_HOVIN	STANDARD:	PR1:	580 AA.
AC	P31976			
DT	01-JUL-1993 (rel. 26, Created)			
DT	01-JUL-1993 (rel. 26, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Ezrin (p81) (Cytovillin) (Willin 2).			
GN	VIL2.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI:taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	ISSUE-Brain;			
RA	Bergson C.M., Zhao H., Salih K., Duman R.S., Nestler E.J.;			
RT	"Ezrin and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus."			
RT	Cell. Mol. Neurosci. 4:64-73(1993).			
RN	[2]			
RP	SEQUENCE OF 1-15 AND 126-140.			
RC	TISSUE-Kidney;			
KX	MEDLINE 96239137; PubMed-8660651;			
RA	Galat A., Gerbed M.C., Bozet F., Riviere S.;			
RT	"Ezrin and plectin, and their amino acid compositions, uniqueness, variability, and applications."			
RT	Arch Biochem Biophys. 330:229-237(1996).			
CC	FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.			
CC	SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN (CYTOPLASMIC SIDE).			
CC	PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.			
CC	SIMILARITY: CONTAINS 1 BAND 4 1-LIKE DOMAIN.			
CC	THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in the way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib.ch">license@sib.ch</a> ).			
DR	EMBL; M98498; AAA040510.1;			
DR	InterPro; IPR000299; Band4.1.			
DR	InterPro; IPR000798; Ezrad/moesin.			
DR	Pfam; PF00373; Band_41; 1.			
DR	Pfam; PF00769; PRM; 1.			
DR	PRINTS; PR009435; HAND41.			
DR	SMART; SM00295; H41; 1.			
DR	PROSITE; PS00660; BAND_41_1; 1.			
DR	PROSITE; PS00661; BAND_41_2; 1.			
DR	PROSITE; PS00657; BAND_41_3; 1.			
KW	Structural protein, Cytoskeleton, Phosphorylation.			
FT	INIT_MET 0			

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FI DOMAIN 57 224 BAND 4.1-LIKE.
FI MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
FI MOD_RES 353 353 (BY SIMILARITY)
FI MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
FI MOD_RES 353 353 (BY SIMILARITY)
SQ SEQUENCE 580 AA: 68629 MW: 6CD6635C200FAA3 CRG64;

Query Match 100.0%; Score 69; DR 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMRKEEL 14
DD 333 EREKQMMRKEEL 346

RESULT 2
EZRI_HUMAN
ID EZRI_HUMAN STANDARD; PRI; 585 AA.
AC P15111; P23714; Q9NSJ4.
DT 01-APP-1996 (Rel. 14, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ezrin (p81) (Cytovillin) (Villin 2).
GN Vill2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE-90076135; PubMed-2591371;
RA Gould K.L., Bretscher A., Esch F.S., Hunter T.;
RT "cDNA cloning and sequencing of the protein-tyrosine kinase
RT substrate, ezrin, reveals homology to band 4.1.";
RL EMBO J. 8:4133-4142(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-Placenta;
RA Turunen O., Winkvist P., Pakkanen R., Grzeschik K.-H., Wahlstroem T.,
RA Valeri A.;
RI "Cytovillin, a microvillar Mr 75,000 protein, cDNA sequence,
RI prokaryotic expression, and chromosomal localization.";
RL J. Biol. Chem. 264:16727-16732(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Ottenwälder H., Germaier H., Mewes H. W., Weil R., Wiemann S.;
RI Submitted (MAP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 171-179 AND 342-349.
RX MEDLINE-9611348; PubMed-8713105;
RA Egeron M., Merity P. J., Decker E., Kelso A., Simpson P. J.;
RI "Identification of the 70kD heat shock cognate protein (Hsc70) and
RI alpha-actinin-1 as novel phosphotyrosine containing proteins in T
RI lymphocytes.";
RL Biochem. Biophys. Res. Commun. 224:666-674(1996).
RN [5]
RP PHOSPHORYLATION BY PDGFR.
RX MEDLINE-92406868; PubMed-1382070;
RA Krieg J., Hunter T.;
RI "Identification of the two major epidermal growth factor induced
RI tyrosine phosphorylation sites in the microvillar core protein
RI ezrin.";
RL J. Biol. Chem. 267:19258-19265(1992).
RN [6]
RP PHOSPHORYLATION.
RX MEDLINE-92388649; PubMed-1381389;
RA Egeron M., Burgess W. H., Chen D., Decker P. J., Bretscher A.,
RA Samuelson L.E.;
RI "Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein
RI in T cells.";
RL J. Immunol. 149:1847-1852(1992).

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-1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
-1- STRUCTURES TO THE PLASMA MEMBRANE.
-1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
(CYTOPLASMIC SIDED).
-1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
EPITHELIAL CELLS.
-1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
-1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
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CC
EMBL: X51521; CAA35893.1;
EMBL: J05021; AAA61278.1; ALT_INIT.
EMBL: A1162086; CAA82418.1; ALT_INIT.
PIR: S09263; S09263.
PIR: A34400; A34400.
SWISS-2DPAGE: P15311; HUMAN.
GeneW: HNC:12691; Vill2.
MIM: 123900;
InterPro: IPR000299; Hand_4.1.
InterPro: IPR000798; Ez/tad/moesin.
Pfam: PF00373; Band_4.1; 1.
Pfam: PF00769; ERM_1; 1.
PRINTS: PR00935; HAND41.
SMART: SM00295; H41; 1.
PROSITE: PS00660; HAND_4.1; 1.
PROSITE: PS00661; BAND_4.1; 1.
PROSITE: PS00507; BAND_4.1; 1.
KW Structural protein; Cytoskeleton; Phosphorylation.
FT INIT_MET 0
FT DOMAIN 57 224 HAND 4.1-LIKE.
FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR).
FT MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR).
FT CONFLICT 531 531 V -> L (IN REF. 3).
SQ SEQUENCE 585 AA: 69267 MW: 2A844D140E3B0ACC CRG64;

Query Match 100.0%; Score 69; DR 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMRKEEL 14
DD 333 EREKQMMRKEEL 346

RESULT 3
EZRI_MOUSE
ID EZRI_MOUSE STANDARD; PRI; 585 AA.
AC P26040;
DE 01-MAY-1992 (Rel. 22, Created)
DE 01-MAY-1992 (Rel. 22, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ezrin (p81) (Cytovillin) (Villin 2).
GN Vill2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92064635; PubMed-1955455;
RA Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
RI "Ezrin is a novel member of the band 4.1 family.";
RL J. Cell Biol. 115:1039-1048(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
-1- SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC EPITHELIAL CELLS.
CC -1- PTM: PHOSPHORYLATED BY PROTRIN-TYROSINE KINASES.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN
CC
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CC
CC EMBL: X60671; CAA43086.1;
CC FIRM: B41129; B41129.
CC MGI: MGI:98941; V112.
CC InterPro: IPR000299; Band 4.1
CC InterPro: IPR000798; Ez/rad/moesin.
CC Pfam: PF00373; Band_41; 1.
CC Pfam: PF00769; FRM; 1.
CC PRINTS: PR00935; BAND41.
CC SMART: SM00295; B41; 1.
CC PROSITE: PS00660; BAND_41_1; 1.
CC PROSITE: PS00661; BAND_41_2; 1.
CC PROSITE: PS00557; BAND_41_3; 1.
CC PROSITE: PS00557; BAND_41_3; 1.
CC Structural protein; Cytoskeleton; Phosphorylation.
CC INIT_MET 0 0 BY SIMILARITY.
CC D_MAIN 57 224 BAND 4.1-LIKE.
CC MOD_RES 145 145 PHOSPHORYLATION (BY PDGFP)
CC MOD_RES 353 353 PHOSPHORYLATION (BY PDGFP)
CC MOD_RES 353 353 PHOSPHORYLATION (BY SIMILARITY).
CC MOD_RES 353 353 PHOSPHORYLATION (BY SIMILARITY).
CC SEQUENCE 585 AA; 69214 MW; 2057E2EEB095D2 CRC64.
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CC Query Match 95.78; Score 66; DB 1; Length 585;
CC Best Local Similarity 92.98; Pred. No. 0.036;
CC Matches 13, Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EREKQMMREKEEL 14
CC ID 333 EREKQMMREKEEL 346
CC
CC RESULT 4
CC MOES_HUMAN STANDARD; PRT; 576 AA.
CC P26038;
CC DT 01-MAY-1992 (Rel. 22, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Moesin (Membrane-organizing extension spike protein).
CC GN MSN.
CC OS Homo sapiens (Human).
CC CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
CC CC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
CC CC NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-15; 54-59 AND 413-424
CC RC TISSUE-Placenta;
CC RX MEDLINE=9220240; PubMed=1924289;
CC RA Lankes W.T., Furthmayr H.;
CC RT "Moesin, a member of the protein 4.1-talin-cytin family of proteins.";
CC PL Proc Natl Acad Sci U S A 88:8297-8301(1991)
CC RN [2]
CC PP SEQUENCE FROM N.A.
CC RA Howden P.;
CC RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: IN ALL TISSUES AND CULTURED CELLS STUDIED.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- DATABASE: NAMP-Atlas Genet Cytogenet Oncol Haematol;
CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/MSN0363.htm".

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CC
CC EMBL: M57606; AAA36322.1;
CC FIRM: 798046; GAR46479.1;
CC PIR: A41289; A41289.
CC Aarhus/Ghent-2DPAGE; 3515; IFF.
CC Aarhus/Ghent-2DPAGE; 3516; IFF.
CC Genew. RGN: 7373; MSN.
CC MIN: 309845;
CC InterPro: IPR000299; Band 4.1.
CC InterPro: IPR000798; Ez/rad/moesin.
CC Pfam: PF00373; Band_41; 1.
CC Pfam: PF00769; FRM; 1.
CC PRINTS: PR00935; BAND41.
CC SMART: SM00295; B41; 1.
CC PROSITE: PS00660; BAND_41_1; 1.
CC PROSITE: PS00661; BAND_41_2; 1.
CC PROSITE: PS00557; BAND_41_3; 1.
CC PROSITE: PS00557; BAND_41_3; 1.
CC Structural protein; Cytoskeleton.
CC INIT_MET 0 0 BAND 4.1-LIKE.
CC D_MAIN 57 224 BAND 4.1-LIKE.
CC SEQUENCE 576 AA; 67689 MW; 96CE7C38D55A8176 CRC64.
CC
CC Query Match 73.98; Score 51; DB 1; Length 576;
CC Best Local Similarity 71.48; Pred. No. 3.9;
CC Matches 10, Conservative 3; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 EREKQMMREKEEL 14
CC ID 333 EREKQMMREKEEL 346
CC
CC RESULT 5
CC MOES_MOUSE STANDARD; PRT; 576 AA.
CC P26041;
CC DT 01-MAY-1992 (Rel. 22, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Moesin (Membrane-organizing extension spike protein).
CC GN MSN.
CC OS Mus musculus (Mouse).
CC CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
CC CC Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
CC CC NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=93055012; PubMed=1429901;
CC RA Sato N., Funayama N., Nagafuchi A., Yonekura S., Tsukita S.,
CC RA Tsukita S.;
CC RT "A gene family consisting of ezrin, radixin and moesin. Its specific
CC RT localization at actin filament/plasma membrane association sites.";
CC RL J. Cell Sci. 103:131-143(1992).
CC RN [2]
CC RP SEQUENCE OF 11-576 FROM N.A.
CC RX MEDLINE=92243764; PubMed=1573844;
CC RA Furthmayr H., Lankes W.T., Amieva M.R.;
CC RT "Moesin, a new cytoskeletal protein and constituent of filopodia: its
CC RT role in cellular functions.";
CC RL Kidney Int. 41:665-670(1992).
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC
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EMBL: S47577; AAA11762.1; -  
EMBL: M86390; AAA39728.1; -  
MGD: MGI:97167; Msn.  
InterPro: IPR000299; Band\_4.1.  
InterPro: IPR000798; Ez/rad/moesin.  
Pfam: PF00373; Band\_41; 1.  
Pfam: PF00769; Band\_41; 1.  
PRINTS: PR00935; BAND41.  
SMART: SM00295; B41; 1.  
PROSITE: PS00660; BAND\_41\_1; 1.  
PROSITE: PS00661; BAND\_41\_2; 1.  
PROSITE: PS00557; BAND\_41\_3; 1.  
Structural protein; Cytoskeleton.  
FT INIT-MET 0 BY SIMILARITY.  
FT DOMAIN 57 224 BAND 4.1-LIKE.  
SEQUENCE 576 AA: 67529 MW: 3CE0BF7E5F75E6B CRC64:  
Query Match 73.9%; Score 51; DB 1; Length 576;  
Best Local Similarity 71.4%; Pred. No. 3.9;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EREKEOMREKEEL 14  
ID 333 EKEKEIEREKEEL 346  
ID 333 EKEKEIEREKEEL 346

RESULT 6  
MOES\_PIG STANDARD; PRT; 576 AA.  
DI 01-MAY-1992 (Rel. 22, Created)  
DI 01-AUG-1992 (Rel. 23, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Moesin (Membrane organizing extension spike protein).  
GN MSN.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
FN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-94092743; PubMed 8268231;  
RA Larkes W.T., Schwartz Albiez K., Furlmayr H.,  
RT Cloning and sequencing of porcine moesin and radixin cDNA and  
RT identification of highly conserved domains.\*;  
RL Biochim. Biophys. Acta 1216:479-482(1993).  
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL  
CC STRUCTURES TO THE PLASMA MEMBRANE  
CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.  
CC  
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EMBL: M86450; AAB02864.1; -  
PIR: S39804; S39804.  
InterPro: IPR000299; Band\_4.1.  
InterPro: IPR000798; Ez/rad/moesin.  
Pfam: PF00373; Band\_41; 1.  
Pfam: PF00769; ERM; 1.  
PRINTS: PR00935; BAND41.  
Query Match 73.9%; Score 51; DB 1; Length 576;  
Best Local Similarity 71.4%; Pred. No. 3.9;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EREKEOMREKEEL 14  
ID 333 EKEKEIEREKEEL 346  
ID 333 EKEKEIEREKEEL 346

SMART: SM00295; B41; 1.  
PROSITE: PS00660; BAND\_41\_1; 1.  
PROSITE: PS00661; BAND\_41\_2; 1.  
PROSITE: PS00557; BAND\_41\_3; 1.  
Structural protein; Cytoskeleton.  
FT INIT-MET 0 BY SIMILARITY.  
FT DOMAIN 57 224 BAND 4.1-LIKE.  
SEQUENCE 576 AA: 67529 MW: 3CE0BF7E5F75E6B CRC64:

Query Match 73.9%; Score 51; DB 1; Length 576;  
Best Local Similarity 71.4%; Pred. No. 3.9;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKEOMREKEEL 14  
ID 333 EKEKEIEREKEEL 346  
ID 333 EKEKEIEREKEEL 346

RESULT 7  
RADL\_HUMAN STANDARD; PRT; 583 AA.  
DI 01-FEB-1994 (Rel. 28, Created)  
DI 01-FEB-1994 (Rel. 28, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Radixin.  
GN RDX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
FN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-93252378; PubMed-8486357;  
RA Wilgenbus K.K., Milatovich A., Francke U., Furlmayr H.,  
RT Molecular cloning, cDNA sequence, and chromosomal assignment of the  
RT human radixin gene and two dispersed pseudogenes.\*;  
RL Genomics 16:199-205(1993).  
CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE  
CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE  
CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCUT OF THE  
CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE  
CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.  
CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.  
CC  
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EMBL: L03320; AAA36541.1; -  
PIR: A46127; A46127; 2501; IEF.  
Aarhus/Chent-2DPAGE; RDX.  
Genew: H0NC:9944; RDX.  
MIM: 179410;  
InterPro: IPR000299; Band\_4.1.  
InterPro: IPR000798; Ez/rad/moesin.  
Pfam: PF00373; Band\_41; 1.  
Pfam: PF00769; ERM; 1.  
PRINTS: PR00935; BAND41.  
SMART: SM00295; B41; 1.  
PROSITE: PS00660; BAND\_41\_1; 1.  
PROSITE: PS00661; BAND\_41\_2; 1.  
PROSITE: PS00557; BAND\_41\_3; 1.  
Structural protein; Cytoskeleton; Actin-binding; Capping protein.  
FT DOMAIN 58 225 BAND 4.1-LIKE.  
FT SEQUENCE 583 AA: 68564 MW: 889687E1D675FE7 CRC64:

Query Match 73.98; Score 51; DB 1; Length 583;  
 Best Local Similarity 71.48; Pred. No. 4;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14  
 1:||||:|||||  
 DB 334 EREKRIEREKEEL 347

## RESULT 8

1D RAD1\_MOUSE STANDARD; PRT; 583 AA.  
 AC P26043;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Radixin  
 GN RDX  
 OS Mus musculus (Mouse)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
 CC NCBI\_TaxID-10090;  
 RN [1]  
 PP SEQUENCE FROM N.A. AND SEQUENCE OF 28-53 AND 263-277.  
 KC TISSUE=LIVER;  
 RA MEDLINE-92054635; PubMed-1955155;  
 RA Funayama N., Naituchi A., Sato N., Tsukita S., Tsukita S.;  
 FT "Radixin is a novel member of the Band 4.1 family."  
 RL J. Cell Biol. 115:1039-1048(1994).  
 CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE  
 CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE  
 CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE  
 CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.  
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN

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EMBL: X60672; cDNA 1087 1;  
 DR PIR: A41129; A41129.  
 DR MGD: MGI-97887; Pdx.  
 DR InterPro: IPR000299; Pdx.  
 DR InterPro: IPR000798; P2/rad/moesin.  
 DR Pfam: PF00173; Band.41; 1.  
 DR Pfam: PF00769; ERM; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00295; B41; 1.  
 DR PROSITE: PS00660; BAND\_41\_1; 1.  
 DR PROSITE: PS00661; BAND\_41\_2; 1.  
 DR PROSITE: PS00507; BAND\_41\_3; 1.  
 KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.  
 FT DOMAIN 58 225  
 FT DOMAIN 470 477  
 FT DOMAIN 583 AA; 3219A52ECDC71BE CRC64;  
 SQ SEQUENCE 583 AA; 68451 MW; 3219A52ECDC71BE CRC64;

Query Match 73.98; Score 51; DB 1; Length 583;  
 Best Local Similarity 71.48; Pred. No. 4;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14  
 1:||||:|||||  
 DB 334 EREKRIEREKEEL 347

## RESULT 9

1D RAD1\_PIG STANDARD; PRT; 583 AA.  
 AC P26043;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Radixin  
 GN RDX  
 OS Sus scrofa (Pig)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;  
 CC NCBI\_TaxID-9823;  
 RN [1]  
 PP SEQUENCE FROM N.A.

AC P26044;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Radixin (Moesin B)  
 GN RDX

OS Sus scrofa (Pig)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;  
 CC NCBI\_TaxID-9823;  
 RN [1]  
 PP SEQUENCE FROM N.A.

KA Laikes W.L., Schwartz Albiez R., Fathallah H.;  
 FT "Cloning and sequencing of porcine moesin and radixin cDNA and  
 PT identification of highly conserved domains."  
 PI Biochim Biophys Acta 1216:479-482(1993).

CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE  
 CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE  
 CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE  
 CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.

CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN

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EMBL: M66444; AAR02865.1;  
 DR PIR: S39805; S39805.  
 DR InterPro: IPR000299; Band.4.1.  
 DR InterPro: IPR000798; P2/rad/moesin.

DR Pfam: PF00173; Band.41; 1.  
 DR Pfam: PF00769; ERM; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00295; B41; 1.  
 DR PROSITE: PS00660; BAND\_41\_1; 1.  
 DR PROSITE: PS00661; BAND\_41\_2; 1.  
 DR PROSITE: PS00507; BAND\_41\_3; 1.

KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.  
 FT DOMAIN 58 225  
 FT DOMAIN 470 477  
 FT DOMAIN 583 AA; 59A286DCAF7397 CRC64;  
 SQ SEQUENCE 583 AA; 68549 MW; 59A286DCAF7397 CRC64;

Query Match 73.98; Score 51; DB 1; Length 583;  
 Best Local Similarity 71.48; Pred. No. 4;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14  
 1:||||:|||||  
 DB 334 EREKRIEREKEEL 347

RESULT 10  
 1D TRHY\_SHEEP STANDARD; PRT; 1549 AA.  
 AC P22793;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Trichohyalin

GN THH  
 OS Ovis aries (Sheep)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis;  
 CC NCBI\_TaxID-9940;  
 RN [1]  
 PP SEQUENCE FROM N.A.





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FI NON_TER 421 321
SQ SEQUENCE 321 AA: 37805 MW: 08844A068190714H CRC64:

Query Match 62.3% Score 43: DB 1: Length 321;
Best Local Similarity 61.5% Pred. No. 27;
Matches 8: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EREKQMMREKEE 13
   1:||||:|||||
DB 290 EKEKEKEKEKE 302

RESULT 13
ABRA_PLAFC
ID ABRA_PLAFC STANDARD; PRT: 743 AA.
AC P25620;
UT 01-AUG-1991 (Rel. 19, Created)
DI 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE 101 kDa malaria antigen (PIU1) (Acidic basic repeat antigen).
GN ABRA.
OS Plasmodium falciparum (isolate Camp / Malaysia)
OC Eukaryota; Alveolata; Apicomplexa; Baemosporida; Plasmodium.
OX NCBI_TaxID=5835;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86298794; PubMed=3042768;
RA Weber J.L., Lyon T.A., Wolff P.H., Chalay J.D.;
RT "Primary structure of a Plasmodium falciparum malaria antigen located at the merozoite surface and within the parasitophorous vacuole."
RL J. Biol. Chem. 263:11421-11425(1988).
CC -!- SURCELLULAR LOCATION: AT THE MEROZOITE SURFACE AND WITHIN THE PARASITOPHOUS VACUOLE.
CC -!- PTM: NOT GLYCOSYLATED (PROBABLE).
CC
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CC
DR EMBL: J03902; AAA29462.1;
DR PIR: A29232; A29232.
KW Antigen; Malaria; Repeat.
FT DOMAIN 226 273 8 X 5 AA REPEATS OF [VT]-N-D [ED] [ED]-D.
FT REPEAT 226 231
FT REPEAT 232 237
FT REPEAT 238 243
FT REPEAT 244 249
FT REPEAT 250 255
FT REPEAT 256 261
FT REPEAT 262 267
FT REPEAT 268 273
FT DOMAIN 674 731 TANDEM REPEATS OF K-E(2-3).
SQ SEQUENCE 743 AA: 86622 MW: FBF0BF8B07D922C CRC64:

Query Match 62.3% Score 43: DB 1: Length 743;
Best Local Similarity 61.5% Pred. No. 62;
Matches 8: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EREKQMMREKEE 13
   1:||||:|||||
DB 694 EKEKEKEKEKE 706

RESULT 14
YLR2_HUMAN
ID YLR2_HUMAN STANDARD; PRT: 1157 AA.
AC Q14687;
DI 01-NOV-1997 (Rel. 35, Created)
DE 01-NOV-1997 (Rel. 35, Last sequence update)

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DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0182 (Fragment).
GN KIAA0182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 3:17-24(1996).
CC
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CC
DR EMBL: D80004; HA011499.1;
KW Hypothetical protein.
FT NCN_TER 1
FT DOMAIN 591 596 POLY-PRO.
FT DOMAIN 685 688 POLY-ARG.
FT DOMAIN 1042 1047 POLY-GLU.
SQ SEQUENCE 1157 AA: 130323 MW: B01A0AF5A6FAH5FH CRC64:

Query Match 62.3% Score 43: DB 1: Length 1157;
Best Local Similarity 64.3% Pred. No. 97;
Matches 9: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EREKQMMREKEE 14
   1:||||:|||||
DB 326 ERQPEQAREKEE 339

RESULT 15
IF3A_MOUSE
ID IF3A_MOUSE STANDARD; PRT: 1344 AA.
AC P23116; Q60697; Q62162;
DI 01-NOV-1991 (Rel. 20, Created)
DE 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (p162 protein) (Centrosomin).
GN EIF3S10 OP EIF3 OR CSNA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoma;
RA Fisher R., Fillmore H., Reynolds A.H.;
RT "Molecular cloning and characterization of the 16.2 kDa component of a multi-protein complex phosphorylated by Src."
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 514-961 FROM N.A. (CENTROSOMIN B).
RX MEDLINE=98039715; PubMed=9372446;
RA Petzelt C., Joswig G., Mineheva A., Bucher P., Stammer H., Werner D.;
RT "The centrosomal protein centrosomin A and the nuclear protein centrosomin B derive from one gene by post-transcriptional processes involving RNA editing."
RL J. Cell Sci. 110:2573-2578(1997).
RN [3]
RP SEQUENCE OF 514-790 FROM N.A. (CENTROSOMIN A).

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RX MEDLINE-91277032; PubMed-1829085;
RA Joswig G., Petzelt C., Werner D.;
RT "Murine cDNAs coding for the centrosomal antigen centrosomin A.";
RL J. Cell Sci. 98:37-43(1991).
RN [4]
RP REVISIONS.
RA Joswig G., Petzelt C., Werner D.;
RU Submitted (DEC 1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MENA.
CC -!- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
CC -!- SUPRACELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
CC -----
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CC -----
DR FMBL: U14172; AAA90910.1; -;
DR FMBL: X84651; CAA59144.1; -;
DR FMBL: X17373; CAA35246.1; -;
DR PIR: S13800; S13800.
DR MGD: MGI:95301; E113.
DR InterPro: IPR000717; pET
DR InterPro: IPR002017; Spectrin.
DR Pfam: PF01399; PCI_1.
DR SMART; SM00088; PIN7; 1.
KW Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.
FT DOMAIN 924 1133
FT [GP]-[PS]-[RW]-R-[GN]-[AM].
FT HQEAKEREKILQERFQKKIVREKLEQIKKTE ->
FT PRKGAREGTNPSTRIRANQFENGSGAVRAQDEIR (IN
FT REF. 2 AND 3).
FT EL -> DY (IN REF. 2 AND 3).
FT Q -> H (IN REF. 2 AND 3).
FT A -> V (IN REF. 2 AND 3).
FT RHR -> SIVA (IN REF. 3).
FT E -> D (IN REF. 2).
FT SQ SEQUENCE 1344 AA; 161949 MW; F4CAE2169F577712 CRC64;
Query Match 62.3%; Score 43; DB 1; Length 1344;
Best Local Similarity 50.0%; Pred. No. 1.le+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Caps 0;
QY 1 EREKQMMREKREL 14
Db 618 EREKERILQEHQI 631

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Search completed: January 16, 2003, 16:51:09  
Job time : 22.4 secs

